AMENDMENTS TO THE CLAIMS:

This listing of the claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. *(**currently** amended)* A method for providing an integrated genetic and physical map of a genome or a part thereof, the method comprising the steps of:

(a) providing at least two individual genetic markers for the genome or a part thereof in the form of a genetic map;

(b) identifying at least one AFLP fragment characterizing each genetic marker by means of AFLP fingerprinting, employing at least one forward AFLP primer and at least one reverse AFLP primer;

(c) providing a library of clones comprising fragments of the genome or a part thereof, which is an artificial chromosome library;

(d) pooling individual clones in the library to generate ~~generating~~ a multitude of pools, each pool containing a multitude of individual clones from the library;

(e) generating an AFLP fingerprint for each of the pools employing forward AFLP primers and reverse AFLP primers;

(f) identifying in the multitude of pools a pool in which an AFLP fragment that was identified in step (b) is present in the fingerprint of the pool;

(g) generating an AFLP fingerprint for each of the individual clones in the pool identified in step (f) employing forward AFLP primers and reverse AFLP primers, and identifying the clone containing the AFLP fragment identified in step (b) in such clone's AFLP fingerprint;

(h) ~~generating a contig comprising~~ aligning the individual clone identified in step (g) to generate a contig;

(i) repeating steps (f) - (h) for at least a second AFLP fragment identified in step (b) whereby the second, or a further, AFLP fragment characterizes a second, or a further, genetic marker; and,

(j) linking at least two contigs obtained in step (h);

thereby obtaining said integrated genetic and physical map of the genome or a part thereof, which comprises at least two genetic markers; wherein:

(1) the forward AFLP primers used in steps (b) and (e) comprise K selective nucleotides at the 3'-end,

(2) the reverse AFLP primers used in steps (b) and (e) comprise L selective nucleotides at the 3'-end,

(3) the forward AFLP primers used in step (g) comprise M selective nucleotides at the 3'-end, and

(4) the reverse AFLP primers used in step (g) comprise N selective nucleotides at the 3' end, and

wherein K, L, M, N are integers with a value from 0 to 10, and wherein the forward and reverse AFLP primers used in steps (b) and (e) are of higher selectivity, and the forward and reverse AFLP primers used in step (g) are of lower selectivity ~~(K+L) > (M+N)~~.

2. *(**currently** amended)* A method for linking a genetic marker to a physical marker in a genome or a part thereof, the method comprising the steps of:

(a) characterizing the genetic marker by means of at least one AFLP fragment identified through AFLP fingerprinting employing at least one forward AFLP primer and at least one reverse AFLP primer;

(b) providing a library of clones comprising fragments of the genome or a part thereof which is an artificial chromosome library;

(c) pooling individual clones in the library to generate ~~generating~~ a multitude of pools, each pool containing a multitude of individual clones from the library;

(d) generating an AFLP fingerprint for each of the pools employing forward AFLP primers and reverse AFLP primers;

(e) identifying in the multitude of pools a pool in which an AFLP fragment identified in step (a) is present in the fingerprint of the pool;

(f) generating an AFLP fingerprint for each of the individual clones in the pool identified in (e) employing forward AFLP primers and reverse AFLP primers, and identifying the clone containing the AFLP fragment identified in (a) in its AFLP fingerprint;

(g) ~~generating a contig comprising~~ aligning the individual clone identified in step (f) to generate a contig,

thereby linking the genetic marker to a physical marker;

wherein

(1) the forward AFLP primers used in steps (a) and (d) comprise K selective nucleotides at the 3'-end,

(2) the reverse AFLP primers used in steps (a) and (d) comprise L selective nucleotides at the 3'-end,

(3) the forward AFLP primers used in step (f) comprise M selective nucleotides at the 3'-end, and

(4) the reverse AFLP primers used in step (f) comprise N selective nucleotides at the 3' end, and

wherein K, L, M, N are integers with a value from 0 to 10, and wherein the forward and reverse AFLP primers used in steps (b) and (e) are of higher selectivity, and the forward and reverse AFLP primers used in step (g) are of lower selectivity~~(K+L) > (M+N)~~.

3. *(previously presented)* The method according to claim 2, wherein steps (a)-(g) are repeated for additional genetic markers in the genome or a part thereof and wherein the contigs obtained in (g) are aligned to obtain an integrated physical and genetic map.

4. ***(currently** amended)* The method according to claim 1 , wherein the AFLP primers used in steps (b) and (e) have in total ~~sum (K+L) minus the sum (M+N) is~~ at least 2 more selective nucleotides than the AFLP primers used in step (g).

5. ***(currently** amended)* The method according to claim 4, wherein the AFLP primers of lower selectivity have ~~sum M+N is~~ at least 0 selective nucleotides.

6. *(currently amended)* The method according to claim 5, wherein each pool contains at most 0.6 genome equivalents of the total genome being analyzed .

7. *(currently amended)* The method according to claim 6, further comprising an additional pooling step.

8. *(currently amended)* The method according to claim 7 , wherein the genetic markers are provided with a density of at least one genetic marker per 100 kb.

9. ***(currently** amended)* The method according to claim 8, wherein the contigs are generated ~~aligned~~ using a computer program suitable for ~~such~~ said aligning.

10. *(currently amended)* The method according to claim 9, wherein the artificial chromosome library contains at least 5 genome equivalents.

11. to 14. (Canceled)

15. *(previously presented)*. The method according to claim 1, wherein the artificial chromosome library is a BAC library or a YAC library.

16. *(previously presented)*. The method according to claim 2, wherein the artificial chromosome library is a BAC library or a YAC library.

17. ***(currently** amended)* The method according to claim 1, wherein the AFLP primers used in steps (b) and (e) have in total sum ~~(K+L) minus the sum (M+N) is at least~~ at least 3 more selective nucleotides than the AFLP primers used in step (g).

18. ***(currently** amended)* The method according to claim 1, wherein the AFLP primers used in steps (b) and (e) have in total ~~sum (K+L) minus the sum (M+N) is at least~~ at least 4 selective nucleotides than the AFLP primers used in step (g).

19. ***(currently** amended)* The method according to claim 4, wherein the AFLP primers of lower selectivity have ~~sum M+N is~~ at least 1 selective nucleotide.

20. ***(currently** amended)* The method according to claim 4, wherein the AFLP primers of lower selectivity have ~~sum M+N is~~ at least 2 selective nucleotides.

21. ***(currently** amended)* The method according to claim 4, wherein the AFLP primers of lower selectivity have ~~sum M+N is~~ at least 3 selective nucleotides.

22. *(previously presented)* The method according to claim 5, wherein each pool contains at most 0.5 genome equivalents of the total genome being analyzed.

23. *(previously presented)* The method according to claim 5, wherein each pool contains at most 0.3 genome equivalents of the total genome being analyzed.

24. ***(currently** amended)* The method according to claim 9~~claim 8~~ wherein the computer program is FPC.